

- 36 -

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

(countries other than US) AMRAD OPERATIONS PTY. LTD.

(us only) Hayward, N and Weber, G

(ii) TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A  
GENETIC SEQUENCE ENCODING SAME

(iii) NUMBER OF SEQUENCES: 14

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DAVIES COLLISON CAVE

(B) STREET: 1 LITTLE COLLINS STREET

(C) CITY: MELBOURNE

(D) STATE: VICTORIA

(E) COUNTRY: AUSTRALIA

(F) ZIP: 3000

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT INTERNATIONAL

(B) FILING DATE: 22-FEB-1996

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: AU PN1457

(B) FILING DATE: 02-MAR-1995

(A) APPLICATION NUMBER: AU PN6647

(B) FILING DATE: 20-NOV-1995

(A) APPLICATION NUMBER: AU PN7274

(B) FILING DATE: 22-DEC-1995

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(C) REFERENCE/DOCKET NUMBER: EJH/EK

(A) TELEPHONE: +61 3 9254 2777

(B) TELEFAX: +61 3 9254 2770

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) **FEATURE:**

(A) NAME/KEY: CDS

(B) LOCATION: 17...589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTT GCC TTG CTG CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG GCT GCA 97  
Leu Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala  
15 20 25

CCC ATG GCA GAA GGA GGA GGG CAG AAT CAT CAC GAA GTG GTG AAG TTC 145  
Pro Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe  
30 35 40

ATG GAT GTC TAT CAG CGC AGC TAC TGC CAT CCA ATC GAG ACC CTG GTG 193  
Met Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val  
45 50 55

GAC ATC TTC CAG GAG TAC CCT GAT GAG ATC GAG TAC ATC TTC AAG CCA 241  
Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro  
60 65 70 75

TCC TGT GTG CCC CTG ATG CGA TGC GGG GGC TGC TGC AAT GAC GAG GGC 289  
Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly  
80 85 90

- 38 -

CTG GAG TGT GTG CCC ACT GAG GAG TCC AAC ATC ACC ATG CAG ATT ATG 337  
 Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met  
 95 100 105

CGG ATC AAA CCT CAC CAA GGC CAG CAC ATA GGA GAG ATG AGC TTC CTA 385  
 Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu  
 110 115 120

CAG CAC AAC AAA TGT GAA TGC AGA CCA AAG AAA GAT AGA GCA AGA CAA 433  
 Gln His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln  
 125 130 135

GAA AAT CCC TGT GGG CCT TGC TCA GAG CGG AGA AAG CAT TTG TTT GTA 481  
 Glu Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val  
 140 145 150 155

CAA GAT CCG CAG ACG TGT AAA TGT TCC TGC AAA AAC ACA GAC TCG CGT 529  
 Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg  
 160 165 170

TGC AAG GCG AGG CAG CTT GAG TTA AAC GAA CGT ACT TGC AGA TGT GAC 577  
 Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp  
 175 180 185

AAG CCG AGG CGG TGAGCCGGGC AGGAGGAAGG AGCCTCCCTC AGCGTTTCGG 629  
 Lys Pro Arg Arg  
 190

GAACCAGATC TCTCACCAGG 649

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50 55 60

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(2) INFORMATION FOR SEQ ID NO:3:

(A) LENGTH: 1094 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) **FEATURE:**

(A) NAME/KEY: CDS  
(B) LOCATION: 3..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CC ATG AGC CCT CTG CTC CGC CGC CTG CTG CTC GCC GCA CTC CTG CAG 47  
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln  
1 5 10 15

CTG GCC CCC GCC CAG GCC CCT GTC TCC CAG CCT GAT GCC CCT GGC CAC 95  
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His  
20 25 30

CAG AGG AAA GTG GTG TCA TGG ATA GAT GTG TAT ACT CGC GCT ACC TGC 143  
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys  
35 40 45

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CAG CCC CGG GAG GTG GTG GTG CCC TTG ACT GTG GAG CTC ATG GGC ACC 191  
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr  
50 55 60

GTG GCC AAA CAG CTG GTG CCC AGC TGC GTG ACT GTG CAG CGC TGT GGT 239  
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly  
65 70 75

GGC TGC TGC CCT GAC GAT GGC CTG GAG TGT GTG CCC ACT GGG CAG CAC 287  
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His  
80 85 90 95

CAA GTC CGG ATG CAG ATC CTC ATG ATC CGG TAC CCG AGC AGT CAG CTG 335  
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu  
100 105 110

GGG GAG ATG TCC CTG GAA GAA CAC AGC CAG TGT GAA TGC AGA CCT AAA 383  
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys  
115 120 125

AAA AAG GAC AGT GCT GTG AAG CCA GAC AGG GCT GCC ACT CCC CAC CAC 431  
Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His  
130 135 140

CGT CCC CAG CCC CGT TCT GTT CCG GGC TGG GAC TCT GCC CCC GGA GCA 479  
Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala  
145 150 155

CCC TCC CCA GCT GAC ATC ACC CAT CCC ACT CCA GCC CCA GGC CCC TCT 527  
Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser  
160 165 170 175

GCC CAC GCT GCA CCC AGC ACC ACC AGC GCC CTG ACC CCC GGA CCT GCC 575  
Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala  
180 185 190

GCT GCC GCT GCC GAC GCC GCA GCT TCC TCC GTT GCC AAG GGC GGG GCT T 624  
Ala Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala  
195 200 205

AGAGCTCAAC CCAGACACCT GCAGGTGCCG GAAGCTGCCA AGGTGACACA TGGCTTTTCA 684

GACTCAGCAG GGTGACTTGC CTCAGAGGCT ATATCCCAGT GGGGGAACAA AGGGGAGCCT 744

GGTAAAAAAC AGCCAAGCCC CCAAGACCTC AGCCCAGGCA GAAGCTGCTC TAGGACCTGG 804

GCCTCTCAGA GGGCTCTTCT GCCATCCCTT GTCTCCCTGA GGCCATCATC AAACAGGACA 864

GAGTTGGAAG AGGAGACTGG GAGGCAGCAA GAGGGGTCAC ATACCAGCTC AGGGGAGAAT 924

GGAGTACTGT CTCAGTTTCT AACCCTCTG TGCAAGTAAG CATCTTACAA CTGGCTCTTC 984

CTCCCCTCAC TAAGAAGACC CAAACCTCTG CATAATGGGA TTTGGGCTTT GGTACAAGAA 1044

CTGTGACCCC CAACCCTGAT AAAAGAGATG GAAGGAAAAA AAAAAAAA 1094

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- 41 -

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu  
 1 5 10 15  
 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
 20 25 30  
 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
 35 40 45  
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
 50 55 60  
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
 65 70 75 80  
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
 85 90 95  
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
 100 105 110  
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
 115 120 125  
 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg  
 130 135 140  
 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro  
 145 150 155 160  
 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala  
 165 170 175  
 His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala  
 180 185 190  
 Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala  
 195 200 205

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- 42 -

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 993 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CC ATG AGC CCT CTG CTC CGC CGC CTG CTG CTC GCC GCA CTC CTG CAG 47  
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln  
 1 5 10 15

CTG GCC CCC GCC CAG GCC CCT GTC TCC CAG CCT GAT GCC CCT GGC CAC 95  
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His  
 20 25 30

CAG AGG AAA GTG GTG TCA TGG ATA GAT GTG TAT ACT CGC GCT ACC TGC 143  
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys  
 35 40 45

CAG CCC CGG GAG GTG GTG GTG CCC TTG ACT GTG GAG CTC ATG GGC ACC 191  
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr  
 50 55 60

GTG GCC AAA CAG CTG GTG CCC AGC TGC GTG ACT GTG CAG CGC TGT GGT 239  
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly  
 65 70 75

GGC TGC TGC CCT GAC GAT GGC CTG GAG TGT GTG CCC ACT GGG CAG CAC 287  
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His  
 80 85 90 95

CAA GTC CGG ATG CAG ATC CTC ATG ATC CGG TAG CCG AGC AGT CAG CTG 335  
 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu  
 100 105 110

GGG GAG ATG TCC CTG GAA GAA CAC AGC CAG TGT GAA TGC AGA CCT AAA 383  
 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys  
 115 120 125

AAA AAG GAC AGT GCT GTG AAG CCA GAT AGC CCC AGG CCC CTC TGC CCA 431  
 Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro  
 130 135 140

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ACAAGAACTG TGACCCCCAA CCTGTATAA AGAGATGGAA GGAAAAAAA AAAAAA 937

(2) INFORMATION FOR SEQ ID NO:6:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(D) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
65 70 75 80



- 44 -

Cys	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln
				85					90					95	
Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu	Gly
			100					105					110		
Glu	Met	Ser	Leu	Glu	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys
		115					120					125			
Lys	Asp	Ser	Ala	Val	Lys	Pro	Asp	Ser	Pro	Arg	Pro	Leu	Cys	Pro	Arg
	130					135					140				
Cys	Thr	Gln	His	His	Gln	Arg	Pro	Asp	Pro	Arg	Thr	Cys	Arg	Cys	Arg
145					150					155					160
Cys	Arg	Arg	Arg	Ser	Phe	Leu	Arg	Cys	Gln	Gly	Arg	Gly	Leu	Glu	Leu
				165					170					175	
Asn	Pro	Asp	Thr	Cys	Arg	Cys	Arg	Lys	Leu	Arg	Arg				
			180					185							

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) **FEATURE:**

- (A) NAME/KEY: CDS  
(B) LOCATION: 3..431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CC ATG AGC CCT CTG CTC CGC CGC CTG CTG CTC GCC GCA CTC CTG CAG 47  
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln  
1 5 10 15

CTG GCC CCC GCC CAG GCC CCT GTC TCC CAG CCT GAT GCC CCT GGC CAC 95  
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His  
20 25 30

CAG AGG AAA GTG GTG TCA TGG ATA GAT GTG TAT ACT CGC GCT ACC TGC 143  
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys  
35 40 45

CAG CCC CGG GAG GTG GTG GTG CCC TTG ACT GTG GAG CTC ATG GGC ACC 191  
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr  
50 55 60

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.5	20	55
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	1.5	10	15
Income	15.5	5.5	10	25
Health status	0.5	0.5	0	1
Smoking status	0.5	0.5	0	1
Alcohol consumption	0.5	0.5	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.5	0.5	0	1
Sleep quality	0.5	0.5	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Overall health	0.5	0.5	0	1
Physical activity	0.5	0.5	0	1
Mental health	0.5	0.5	0	1
Social support	0.5	0.5	0	1
Work-life balance	0.5	0.5	0	1
Financial stability	0.5	0.5	0	1
Family harmony	0.5	0.5	0	1
Personal growth	0.5	0.5	0	1
Community involvement	0.5	0.5	0	1
Environmental awareness	0.5	0.5	0	1
Cultural appreciation	0.5	0.5	0	1
Artistic expression	0.5	0.5	0	1
Volunteer work	0.5	0.5	0	1
Charitable contributions	0.5	0.5	0	1
Philanthropic activities	0.5	0.5	0	1
Leadership roles	0.5	0.5	0	1
Networking opportunities	0.5	0.5	0	1
Professional development	0.5	0.5	0	1
Continuous learning	0.5	0.5	0	1
Adaptability to change	0.5	0.5	0	1
Resilience to stress	0.5	0.5	0	1
Emotional stability	0.5	0.5	0	1
Positive outlook	0.5	0.5	0	1
Optimism	0.5	0.5	0	1
Gratitude	0.5	0.5	0	1
Forgiveness	0.5	0.5	0	1
Empathy	0.5	0.5	0	1
Compassion	0.5	0.5	0	1
Kindness	0.5	0.5	0	1
Generosity	0.5	0.5	0	1
Humility	0.5	0.5	0	1
Patience	0.5	0.5	0	1
Perseverance	0.5	0.5	0	1
Determination	0.5	0.5	0	1
Confidence	0.5	0.5	0	1
Self-esteem	0.5	0.5	0	1
Self-love	0.5	0.5	0	1
Self-respect	0.5	0.5	0	1
Self-discipline	0.5	0.5	0	1
Self-control	0.5	0.5	0	1
Self-awareness	0.5	0.5	0	1
Self-reflection	0.5	0.5	0	1
Self-improvement	0.5	0.5	0	1
Personal goals	0.5	0.5	0	1
Life vision	0.5	0.5	0	1
Future planning	0.5	0.5	0	1
Goal setting	0.5	0.5	0	1
Time management	0.5	0.5	0	1
Productivity	0.5	0.5	0	1
Efficiency	0.5	0.5	0	1
Organization	0.5	0.5	0	1
Orderliness	0.5	0.5	0	1
Cleanliness	0.5	0.5	0	1
Neatness	0.5	0.5	0	1
Hygiene	0.5	0.5	0	1
Healthcare	0.5	0.5	0	1
Medical checkups	0.5	0.5	0	1
Medication management	0.5	0.5	0	1
Dietary habits	0.5	0.5	0	1
Exercise routine	0.5	0.5	0	1
Rest and relaxation	0.5	0.5	0	1
Stress management techniques	0.5	0.5	0	1
Mental health resources	0.5	0.5	0	1
Support groups	0.5	0.5	0	1
Therapy sessions	0.5	0.5	0	1
Counseling services	0.5	0.5	0	1
Community resources	0.5	0.5	0	1
Local organizations	0.5	0.5	0	1
Non-profit organizations	0.5	0.5	0	1
Government services	0.5	0.5	0	1
Public facilities	0.5	0.5	0	1
Recreational activities	0.5	0.5	0	1

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GTG GCC AAA CAG CTG GTG CCC AGC TGC GTG ACT GTG CAG CQC TGT GGT 239  
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly  
65 70 75

GGC TGC TGC CCT GAC GAT GGC CTG GAG TCT GTG CCC ACT GGG CAG CAC 287  
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His  
80 85 90 95

CAA GTC CGG ATG CAG ATC CTC ATG ATC CGG TAC CCG AGC AGT CAG CTG 335  
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu  
100 105 110

GGG GAG ATG TCC CTG GAA GAA CAC AGC CAG TGT GAA TGC AGA CCT AAA 383  
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys  
115 120 125

AAA AAG GAC AGT CCT GTG AAG CCA GAT AGG TGC CGG AAG CTG CGA AGC 431  
Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg  
130 135 140

TGACACATGG CTTTTCAGAC TCAGCAGGGT GACTTGCCCTC AGAGGCTATA TCCCAGTGGG 481

GGAAACAAAGG GGAGCCTGGT AAAAAACAGC CAAGCCCCCA AGACCTCAGC CCAGCCAGAA 551

OCTGCTCTAG GACCTGGGCC TCTCAGAGGG CTCTTCTGCC ATCCCTTGTC TCCCTGAGGC 611

CATCATCAAA CAGGACAGAG TTGGAAGAGG AACTGGSAG GCAGCAAGAG GGCTCACATA 671

CCAGCTCAGG GGAGAATGGA GTACTGTCTC AGTTTCTAAC CACTCTGTGC AAGTAAGCAT 731

CTTACAACCTG GCTCTTCTC CCCTCACTAA GAAGACCCAA ACCTCTGCAT AATGGGATTT 791

GGGCTTTGGT ACAAGAACTG TGACCCCCAA CCTGATAAA AGAGATGGAA GGAAAAAAA 851

AAAAAAA 850

- 46 -

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu  
 1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
 20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
 35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
 50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
 65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
 85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
 100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
 115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg  
 130 135 140

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- 47 -

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..305

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CC ATG AGC CCT CTG CTC CGC CGC CTG CTG CTC GCC GCA CTC CTG CAG 47  
 Met Ser Pro Leu Leu Arg Arg Leu Leu Ala Ala Leu Leu Gln  
 1 5 10 15

CTG GCC CCC GCC CAG GCC CCT GTC TCC CAG CCT GAT GCC CCT GGC CAC 95  
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His  
 20 25 30

CAG AGG AAA GTG GTG TCA TGG ATA GAT GTG TAT ACT CGC GCT ACC TGC 143  
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys  
 35 40 45

CAG CCC CGG GAG GTG GTG GTG CCC TTG ACT GTG GAG CTC ATG GGC ACC 191  
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr  
 50 55 60

GTG GCC AAA CAG CTG GTG CCC AGC TGC GTG ACT GTG CAG CGC TGT GGT 239  
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly  
 65 70 75

GGC TGC TGC CCT GAC GAT GGC CTG GAG TGT GTG CCC ACT GGG CAG CAC 287  
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His  
 80 85 90 95

CAA GTC CGG ATG CAG ACC TAAAAAAG GACAGTGCTG TGAAGCCAGA 335  
 Gln Val Arg Met Gln Thr  
 100

CAGGGCTGCC ACTCCCCACC ACCGTCCCCA GCCCGTTCT GTTCCGGGCT GGGACTCTGC 395

CCCCGGAGCA CCCTCCCCAG CTGACATCAC CCATCCCACT CCAGCCCCAG GCCCCTCTGC 455

CCACGCTGCA CCCAGCACCA CCAGCGCCCT GACCCCCGGA CCTGCCGCTG CCGCTGCCGA 515

CGCCGCAGCT TCCTCCGTTG CCAAGGGCGG GGCTTAGAGC TCAACCCAGA CACCTGCAGG 575

TGCCGGAAGC TGCGAAGGTG ACACATGGCT TTCAGACTC AGCAGGGTGA CTTGCCTCAG 635

AGGCTATATC CCAGTGGGGA ACAAAGAGGA GCCTGGTAAA AACCAGCCAA GCCCCAAGA 695

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- 48 -

CCTCAGCCCA GGCAGAAGCT GCTCTAGGAC CTGGGCCTCT CAGAGGGCTC TTCTGCCATC 755  
 CCTTGTCTCC CTGAGGCCAT CATCAAACAG GACAGAGTTG GAAGAGGAGA CTGGGAGGCA 815  
 GCAAGAGGGG TCACATACCA GCTCAGGGGA GAATGGAGTA CTGTCTCAGT TTCTAACCAC 875  
 TCTGTGCAAG TAAGCATCTT ACAACTGGCT CTTC 910

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu 15  
 1 5 10  
 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln 30  
 20 25 30  
 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln 45  
 35 40 45  
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val 60  
 50 55 60  
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly 80  
 65 70 75 80  
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln 95  
 85 90 95  
 Val Arg Met Gln Thr 100

PCT/CA 96/00094

Sub  
 a3  
 cont



- 50 -

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Oligonucleotide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGGGCAGAG GATCCTGGGG CTGTCTGGCC TCACAGCACT

40

Sub  
93  
cont

60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100